



## SEQUENCE LISTING

RECEIVED

NOV 01 2002

RECEIVED

\*110\* Scheifflinger, Friedrich  
Ferschbaumer, Randolph  
Falkner, Falko-Guenter  
Forner, Friedrich

\*111\*

\*112\*

\*114\* US 09/661,992

\*115\* 106

\*117\* PatentIn Ver. 2.1

\*118\* 1

\*119\* 26

\*120\* LNA

\*123\* Artificial Sequence

\*124\*

\*125\* Description of the artificial sequence:primer

\*400\* 1

ctccattttc ttgtccacct tgggtgc

26

\*116\* 1

\*117\* 26

\*118\* LNA

\*123\* Artificial Sequence

\*124\*

\*125\* Description of the artificial sequence:primer

\*400\* 2

ctcgattctc ttgatcaact cagtcct

26

\*110\* 3

\*111\* 34

\*112\* DNA

\*123\* Artificial Sequence

\*124\*

\*125\* Description of the artificial sequence:primer

\*400\* 3

ttgaatgggc acatgcagat ctct

24

\*110\* 4

\*111\* 34

\*112\* LNA

\*123\* Artificial Sequence

\*124\*

\*125\* Description of the artificial sequence:primer

\*400\* 4

ctcattcttg ttgaagctct tgac

24

<210> 5  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 5  
Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr  
1 5 10

<211> 6  
<212> 12  
<213> PRT  
<214> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 6  
Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr  
1 5 10

<211> 7  
<212> 13  
<213> PRT  
<214> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 7  
Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val  
1 5 10

<211> 8  
<212> 13  
<213> PRT  
<214> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 8  
Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val  
1 5 10

<211> 9  
<212> 13  
<213> PRT  
<214> Artificial Sequence

<220>  
<223> Description of the artificial sequence:CDR3 region

<400> 9

Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val  
1 5 10

4110 10  
4111 13  
4112 PPT  
4113 Artificial Sequence

4120  
4123 Description of the artificial sequence:CDR3 region

4130 10  
Val Tyr Gly Phe Gly Trp Gly Tyr Glu Val Asn Asp Tyr  
1 5 10

4110 11  
4111 16  
4112 PPT  
4113 Artificial Sequence

4120  
4123 Description of the artificial sequence:CDR3 region

4130 13  
Glu Glu Glu Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Glu  
1 5 10 15

Glu Glu

4110 12  
4111 18  
4112 PPT  
4113 Artificial Sequence

4120  
4123 Description of the artificial sequence:CDR3 region

4130 13  
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4110 13  
4111 18  
4112 PPT  
4113 Artificial Sequence

4120  
4123 Description of the artificial sequence:CDR3 region

4130 13  
Glu Tyr Gly Glu Gly Tyr Gly Glu Val Asn Glu Tyr Asp Glu Phe Glu  
1 5 10 15

Trp Glu

<210> 14  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of the artificial sequence:CDR3 region

<400> 14  
Val Arg Tyr Arg Asn Arg Tyr Arg Trp Gly Tyr Arg Gly Arg Phe Gly  
1 5 10 15

Asp Glu

<210> 15  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of the artificial sequence:CDR3 region

<400> 15  
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg  
1 5 10 15

Arg Arg

<210> 16  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of the artificial sequence:CDR3 region

<400> 16  
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<210> 17  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of the artificial sequence:CDR3 region

<400> 17  
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg  
1 5 10 15

Arg Arg

42100 18  
42110 18  
42120 PRT  
42130 Artificial Sequence

42200  
42230 Description of the artificial sequence:CDR3 region

44000 18  
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15  
Arg Arg

42100 19  
42110 18  
42120 PRT  
42130 Artificial Sequence

42200  
42230 Description of the artificial sequence:CDR3 region

44000 19  
Arg Arg Arg Ala Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15  
Arg Arg

42100 20  
42110 18  
42120 PRT  
42130 Artificial Sequence

42200  
42230 Description of the artificial sequence:CDR3 region

44000 20  
Arg Arg Arg Glu Ala Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15  
Arg Arg

42100 21  
42110 18  
42120 PRT  
42130 Artificial Sequence

42200  
42230 Description of the artificial sequence:CDR3 region

44000 21  
Arg Arg Arg Glu Gly Ala Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210 22

4211 18

4212 PFT

4213 Artificial Sequence

4220

4223 Description of the artificial sequence:CDR3 region

4400 21

Arg Arg Arg Glu Gly Gly Ala Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210 23

4211 18

4212 PFT

4213 Artificial Sequence

4220

4223 Description of the artificial sequence:CDR3 region

4400 23

Arg Arg Arg Glu Gly Gly Gly Ala Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210 24

4211 18

4212 PFT

4213 Artificial Sequence

4220

4223 Description of the artificial sequence:CDR3 region

4400 24

Arg Arg Arg Glu Gly Gly Gly Tyr Ala Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210 25

4211 18

4212 PFT

4213 Artificial Sequence

4220

4223 Description of the artificial sequence:CDR3 region

4400 25

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Ala Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 26

4211> 18

4212> FRT

4213> Artificial Sequence

4220>

4221> Description of the artificial sequence:CDR3 region

4400> 26

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Ala Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 17

4211> 18

4212> FRT

4213> Artificial Sequence

4220>

4221> Description of the artificial sequence:CDR3 region

4400> 17

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Ala Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 18

4211> 18

4212> FRT

4213> Artificial Sequence

4220>

4221> Description of the artificial sequence:CDR3 region

4400> 18

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Ala Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 19

4211> 16

4212> FRT

4213> Artificial Sequence

4220>

4221> Description of the artificial sequence:CDR3 region

4400> 29

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Ala Asp Arg

1

5

10

15

Arg Arg

<210> 30

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 30

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Ala Arg

1

5

10

15

Arg Arg

<210> 31

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 31

Arg Arg Arg Tyr Val Tyr Asn Gly Trp Gly Tyr Phe Glu Gly Ala Arg

1

5

10

15

Arg Arg

<210> 32

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 32

Arg Arg Arg Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg

1

5

10

15

Arg Arg

<210> 33

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 33



Arg Arg Arg Glu Gly Glu Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 34

4211> 18

4212> PRT

4213> Artificial Sequence

4220

4223> Description of the artificial sequence:CDR3 region

4400 34

Arg Arg Arg Glu Gly Gly Glu Tyr Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 35

4211> 18

4212> PRT

4213> Artificial Sequence

4220

4223> Description of the artificial sequence:CDR3 region

4400> 35

Arg Arg Arg Glu Gly Gly Gly Glu Tyr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 36

4211> 18

4212> PRT

4213> Artificial Sequence

4220

4223> Description of the artificial sequence:CDR3 region

4400> 36

Arg Arg Arg Glu Gly Gly Gly Tyr Glu Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4210> 37

4211> 18

4212> PRT

4213> Artificial Sequence

4220

4223> Description of the artificial sequence:CDR3 region

<400> 37

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Glu Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<210> 38

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:CDR3 region

<400> 38

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Glu Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<210> 39

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:CDR3 region

<400> 39

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Glu Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

<210> 40

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:CDR3 region

<400> 40

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Glu Phe Asp Arg  
1 5 10 15

Arg Arg

<210> 41

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:CDR3 region

<400> 41

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Glu Asp Arg  
1 5 10 15

Arg Arg

<210> 42

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 42

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Glu Arg  
1 5 10 15

Arg Arg

<210> 43

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 43

Arg Arg Arg Gly Glu Tyr Gly Glu Tyr Trp Asn Gly Asp Phe Tyr Arg  
1 5 10 15

Arg Arg

<210> 44

<211> 13

<212> PPT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 44

Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val  
1 5 10

<210> 45

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 45

Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg  
1 5 10

4210: 46

4211: 14

4212: PRT

4213: Artificial Sequence

4220:

4223: Description of the artificial sequence:CDR3 region

4400: 46

Phe Gly Val Gly Tyr Arg Gly Glu Thr Arg Asn Phe Asp Trp  
1 5 10

4410: 47

4411: 18

4412: PRT

4413: Artificial Sequence

4420:

4423: Description of the artificial sequence:CDR3 region

4430: 47

Glu Glu Glu Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Glu  
1 5 10 15

Glu Glu

4440: 48

4441: 18

4442: PRT

4443: Artificial Sequence

4450:

4453: Description of the artificial sequence:CDR3 region

4460: 48

Arg Arg Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg  
1 5 10 15

Arg Arg

4470: 49

4471: 18

4472: PRT

4473: Artificial Sequence

4480:

4483: Description of the artificial sequence:CDR3 region

4490: 49

Arg Arg Arg Phe Gly Val Gly Tyr Gly Glu Thr Asn Phe Asp Trp Arg  
1 5 10 15

Arg Arg

4210> 50  
4211> 57  
4212> DNA  
4213> Artificial Sequence

4220>  
4221> Description of the artificial sequence:primer

4400> 50  
gtatgcacga ctgcgggccg agccggccat gcccsaggts marctgcags agtcwgg 57

4211> 51  
4212> 56  
4213> DNA  
4214> Artificial Sequence

4221>  
4222> Description of the artificial sequence:primer

4401> 51  
gtatgcgaa ctgcggccca gccggccatg gccgaggtgc agcttcagga gtcagg 56

4211> 52  
4212> 56  
4213> DNA  
4214> Artificial Sequence

4222>  
4223> Description of the artificial sequence:primer

4402> 51  
gtatgcgaa ctgcggccca gccggccatg gccgatgtgc agcttcagga gtcagg 56

4210> 53  
4211> 56  
4212> DNA  
4213> Artificial Sequence

4223>  
4224> Description of the artificial sequence:primer

4403> 53  
gtatgcgaa ctgcggccca gccggccatg gccaggtgc agctgaagsa gtcagg 56

4210> 54  
4211> 56  
4212> DNA  
4213> Artificial Sequence

4224>  
4225> Description of the artificial sequence:primer

4404> 54  
gtatgcgaa ctgcggccca gccggccatg gccgaggtgc agctgcacca rtctgg 56

4211> 55

<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccaggtys arctgcagca gcttgg 56

<210> 5'  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccaggtga agctggtgga rcttgg 56

<210> 5'  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccaggttc agcttcagca gtctgg 56

<210> 5'  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccgaagtgc agctgktgga gwctgg 56

<210> 5'  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of the artificial sequence:primer

<400> 5'  
gtcttcgcaa ctggggccca gccggccatg gccagatcc agttgctgca gtctgg 56

<210> 60  
<211> 66  
<212> DNA  
<213> Artificial Sequence

<220>

<210> Description of the artificial sequence:primer

<41> 61

atggtcagag gcgcgcccac ctgaaccgcc tccacctgag gagacggtga ccgtggtccc 60  
atggtccc 61

<110> 61

<111> 6

<112> DNA

<113> Artificial Sequence

<210>

<210> Description of the artificial sequence:primer

<41> 61

atggtcagag gcgcgcccac ctgaaccgcc tccacctgag gagacggtga ccgtggtccc 60

<110> 61

<111> 6

<112> DNA

<113> Artificial Sequence

<210>

<210> Description of the artificial sequence:primer

<41> 61

atggtcagag gcgcgcccac ctgaaccgcc tccacctgag gagactgtga gagtgggtgcc 60

<110> 61

<111> 60

<112> DNA

<113> Artificial Sequence

<210>

<210> Description of the artificial sequence:primer

<41> 61

atggtcagag gcgcgcccac ctgaaccgcc tccacctgca gagacagtga ccagagtccc 60

<110> 64

<111> 60

<112> DNA

<113> Artificial Sequence

<210>

<210> Description of the artificial sequence:primer

<41> 64

atggtcagag gcgcgcccac ctgaaccgcc tccacctgag gagacggtga ctgagggttc 60

<110> 65

<111> 60

<112> DNA

<113> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 65

tggtcagatg ggcgcgcctc tggcggtggc ggatcggaca ttgagctcac ccagtctcca 60

<210> 66

<211> 59

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 66

tggtcagatg ggcgcgcctc tggcggtggc ggatcggaca ttgtgatgac acagtctcc 59

<210> 67

<211> 59

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 67

tggtcagatg ggcgcgcctc tggcggtggc ggatcggatg tktgatgac ccaactcc 59

<210> 68

<211> 59

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 68

tggtcagatg ggcgcgcctc tggcggtggc ggatcggata ttgtgatrac bcaggcwg 59

<210> 69

<211> 59

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 69

tggtcagatg ggcgcgcctc tggcggtggc ggatcggaca ttgtgctgac mcartctcc 59

<210> 70

<211> 59

<212> DNA

<213> Artificial Sequence

<210>

<223> Description of the artificial sequence:primer

<400> 70



ggttcagatg ggcgcgcctc tggcgggtggc ggatcgaaaa wtgtkctcac ccagtcctcc 59

<210> 71

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<40> 71

ggttcagatg ggcgcgcctc tggcgggtggc ggatcgagaa tywggatgac mcagwctcc 59

<210> 71

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 71

ggttcagatg ggcgcgcctc tggcgggtggc ggatcgaaaa ttgtctcac ccagtcctcc 59

<210> 73

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 73

ggttcagatg ggcgcgcctc tggcgggtggc ggatcgatcat tattgcaggt gcttggtgg 59

<210> 74

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 74

gaatcatctt ggcgcgcctc gtttgatttc cagcttggtg cc 42

<210> 75

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 75

gagtcattct ggcgcgcctc gttttatttc cagcttggtc cc 42

<210> 76  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:primer

<401> 76  
agtcattct gcggcgcgcc gttttatttc cagtctggtc cc 42

<210> 77  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:primer

<401> 77  
agtcattct gcggcgcgcc gttttatttc caactttgtc cc 42

<210> 78  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:primer

<401> 78  
agtcattct gcggcgcgcc gtttcagctc cagcttggtc cc 42

<210> 79  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:mychis 6

<401> 79  
gggcgcagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca 60  
aaacactaa taag 74

<210> 80  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<214>  
<215> Description of the artificial sequence:mychis

<401> 80  
atttttatt agtgatggtg atggtgatgt gcgcgcccat tcagatcttc ttctgagatg 60  
agttttgtt ctgc 74

<210> 81

<211> 726  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 61

```
gaggagaagg tggaggagtc tggacotgag ctgaagaagg ctggagagac agtcaagatc 60
tcttcaaggg cttttgggta tatcttcaca aactatggaa tgaactgggt gaagcaggct 120
caggaaaggg gtttaaagtg gatgggctgg ataaacacot acaactggaga gccaacatat 180
ctgtatgact tcaagggaag gtttgccttc tctttggaaa cctctggcag cactgcctat 240
tttgatgaca acaacotcaa aaatgaggac acggctacat atttctgtgc attatatggt 300
aactcccta aggggtttgc ttactggggc caagggaactc tggtcactgt ctctgcaggt 360
ggaggcgggt caggtggggc cgcctctggc ggtgggggat cggatattca gatgacacag 420
tctccaaat tctgtctgt atcagcagga gacagggta ccataacctg caaggccagt 480
cagagtgtga gtaatgatgt agcttggtag caacagaagg cggggcagtc tctaaacta 540
cggatgact atgcatccaa tggctacact ggagtcctg atcgcttcac tggcagtgga 600
tatgggaagg atttcacttt caccatcagg actgtgcagg ctgaagaact ggcagtttat 660
tctctcagg aggattatgg ctctcctccc acgttcggag ggggcaccaa gotggaaatt 720
aaacgg 726
```

<410> 62

<411> 642

<412> PRT

<413> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 62

```
Glu Val Lys Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Leu Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Arg Ala
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Lys Phe
130 135 140

Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
145 150 155 160

Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
```

165

170

175

Ser Pro Lys Leu Leu Met Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val  
160 165 190

Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr  
195 200 205

Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln  
210 215 220

Asp Tyr Gly Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile  
225 230 235 240

Lys Arg

<112> 63

<111> 747

<112> DNA

<113> Artificial Sequence

<120>

<123> Description of the artificial sequence:scFv region

<400> 85

gaagtcagc tggtaggagc tgggggaggc ctagtgaagc ctggagggtc cctgaaactc 60  
tctgtgcag cctctggatt cacttcagt acctatacca tgtcttgggt tgcagagact 120  
tggagaaga ggcctggagt ggctgcacac attagtagtg gtggtagtta cactactat 180  
tcagtcagt tgaggggagc attcaccatc tcagagaca atgccaagaa cactctgtac 240  
tgcacatga gcagcttgaa gtctgaggac acagccatgt attactgtac aagagatggg 300  
gcacaggggt acggttagtag ctttgactac tggggcgaag gcaccactct cacagtctcc 360  
tcagttggag ggggttcagg tggggcgagg tctgggggtg ggggatgca aattgtgctc 420  
accagcttc cactctccct gcctgtcagt ctggagatc aagctctcat ctcttgacga 480  
ctctgtcaga gcattgtaca tagtaatgga aacacctatt tagaatggta cctgcagaaa 540  
tcagtcagt ctccaaagct cctgatctac aaagtctcca accgattctc tggggtcaca 600  
gcacacatca gtggcagtggt atcagggaca gatttcacac tcaagatcag cagagtggag 660  
cttgaggatc tggagttata ttactgcttt caaggctcac atgttcctgt gacgttcggg 720  
gcagtcacca agctggaaat caaacgg 747

<112> 84

<111> 249

<112> PRT

<113> Artificial Sequence

<120>

<123> Description of the artificial sequence:scFv region

<400> 84

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr  
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val  
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val  
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Ser Ser Leu Lys Ser Gln Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95  
 Thr Arg Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr Trp Gly  
 100 105 110  
 Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly  
 115 120 125  
 Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro  
 130 135 140  
 Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg  
 145 150 155 160  
 Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp  
 165 170 175  
 Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val  
 180 185 190  
 Ser Asn Arg Phe Ser Gly Val Pro Asp Lys Phe Ser Gly Ser Gly Ser  
 195 200 205  
 Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu  
 210 215 220  
 Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly  
 225 230 235 240  
 Gly Gly Thr Lys Leu Gln Ile Lys Arg  
 245

4210 - 65

4211 - 747

4212 - DNA

4213 - Artificial Sequence

4214 -

4215 - Description of the artificial sequence: scFv region

4216 - 65

gagggtgcagc ttcaggagtc aggggggagc ttagtgaagc ctggagggtc cctgaaaactc 60  
 tctgtgcag cctctggatt cactttcagt agctatacca tgtcttgggt tgcacagact 120  
 caggagaaga ggtggagtg ggtgcacacc attagtagtg gtggtagttc cactactat 180  
 ccagccagtg tgaagggtcg attcaccatc tcagagagaa atgccaagaa caccctgtac 240  
 ctgcacatga gcagtctgag gtctgaggac acagccatgt attactgtac aagagagggg 300  
 ggtgttttca ccgtcaactg gtacttcgat gtctggggcg cagggaactc ggtcactgtc 360  
 tctgcaggtg gaggcgggtc aggtggggcg gcctctggcg gtggcggatc ggaaaatgtg 420  
 ctcccccagt ctcagcttc ttggctgtg tctctaggcg agagggccac catatcctgc 480  
 adagccagtg aaagtgttga tagttatggt tataatttta tgcactggta tcagcagata 540  
 ccagacagc caccocaaact cctcatctat cgtgcaccca acctagagtc tgggacccct 600  
 ccaggtttca gtggcagtg gtctaggaca gaattcacc tcaccattaa tctgtggag 660  
 gtgtgatggt ttgcaacctt ttactgtcag caaagtaaty aggatccgct cactgtcgg 720  
 actggaaca gactggaaat aaaaagg 747

4210 - 66

4211 - 249

<212> FRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 66

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val  
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Thr Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp  
100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly  
115 120 125

Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser  
130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys  
145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp  
165 170 175

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala  
180 185 190

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser  
195 200 205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val  
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly  
225 230 235 240

Thr Gly Thr Arg Leu Glu Ile Lys Arg  
245

<210> 67

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 67

```
gaggtgacgc ttcaggagtc agggggagggc ttagtgaagc ctggagggtc cctgaaaactc 60
tcctgtgcag cctctggatt catttttagt agttatacca tgccttgggt tcgccaagact 120
ccggagaaga ggtctggagt ggtcgcaacc attagtagtg gtggtagttc cactactat 180
ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 240
ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atcactgtac aagagagggg 300
gtgtgttatt acgtcaactg gtacttggat gtctggggcg caggaccacac totcaccagtc 360
tcctcaggtg gaggcgggtc aggtggggcg gctctggcg gtgggggac ggacattgag 420
ctcaccacgt ctcacagcttc ttggctgtg totctagggc agagggccac catatcctgc 480
agagtcagtg aaagtgttga tagttatggc aagagtttta tgcactggta ccagcagaaa 540
ccagggcagc caccaaaact cctcatctat cgtgcaccca acctagaatc tgggatccct 600
gcaagttca gtggcagtg gtctaggaca gacttcaccc tcaccattaa tcctgtggag 660
gtgatgatg ttgcnaccta ttactgtcag caaagtaatg aggatccct caggttcggt 720
gttgagacca gactggaaat aaaacgg 747
```

<10> 88

<11> 249

<12> PRT

<13> Artificial Sequence

<120>

<123> Description of the artificial sequence:scFv region

<400> 88

```
Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
  1             5             10             15
```

```
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
      20             25             30
```

```
Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
      35             40             45
```

```
Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
      50             55             60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
      65             70             75             80
```

```
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys
      85             90             95
```

```
Thr Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp
      100            105            110
```

```
Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly
      115            120            125
```

```
Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
      130            135            140
```

```
Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
      145            150            155            160
```

```
Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp
      165            170            175
```

```
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
      180            185            190
```

```
Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
```

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val  
310 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly  
235 235 240

Ala Gly Thr Arg Leu Glu Ile Lys Arg  
245

4110-69

4111-2199

4112-DNA

4113-Artificial Sequence

4120-

4123-Description of the artificial sequence:scFv region

4400-89

```

atgaataacc tattgactac ggcagcgcct gaattgttat taactgcggc ccagcccgcc 60
atggcgagag tgaagcttgt gaagtctggg gaaggcttag tgaagcctgg agggctccctg 120
aaactctcct ttgcagcctc ttgatttact ttccagtagc ataccatgct ttgggttcgc 180
tagactcagg aqaapaggtt gaagtgggtc gaaacatta gtagtggngg tagttccacc 240
taactatccag acagtgtgaa gggcgcgttc aacatctcca gagacaatgc caagaatacc 300
ctgtacatgc aaatpaggag tctgaggtct gaggacacag ccatgtatta ctgtacaaga 360
aggggggggtg gtttaccctt aaactgctac ttccatgtct gggcgcgcag aaactccagt 420
accgtctcct caggtggagg cgggtccaggt gggcgcgcct ctgggggttg cggatccgac 480
atttgtctga cacagctctc agcttctcttg gctgtgtctc tagggcagag ggcacacata 540
tccctgcagag ccagtgaag tggtpatagt tatggctata atttctcca ctggatccag 600
tagataccag gacagccacc aaaaactctc atctatcttg caccacaact agagtctcgg 660
atccctgcca ggttcagtg cagtgggtct aggcacagct ccacccctac cattaatcct 720
ctggaggttg atgatgttc aacctattac tctcagcaaa gtaattgagg taacctcacc 780
ttgggtactg gacacagact ggaataaaaa cggcgggcgc cagcccgggc accagaaat 840
cctgttcttg aaaaaccggc tgcacaggc gatattact cacccgggcg tctcgcgcgt 900
ttaaagggtg atcagactgc cgtcttgctt gattctctta cggataaacc tgcataaaat 960
attatcttgc tgattggcga tgggatgggg gactcggaaa ctactgcgcg acgtaattat 1020
gcggaagggt cggcgcgctt ttttaaaggt atagatgctt taccgcttac cgggcaatan 1080
actcaactat cgttgaataa aaaaaccggc aaacccgact accccaaga ctggctgcca 1140
tcagcaaccg cctgttcaac cgggtgtcaaa acctataacg acccgctggg ctccgatata 1200
cagcaaaaag atcaaccaac gattctggaa atggcaaaag ccgcajgtct agcgaccgtt 1260
aacgttctta ccgcagagtt gcaggatgac acccgcgctg cgtgtgtggc acatgtgaca 1320
tcgcgcaaat gctacggtcc gagcgcgacc agtcaaaaat gtcgggttaa cgtcttgcaa 1380
aaaggcggaa aaggatcgat taccgaacag ctgtttaacg ctctgtccca cgttacgctt 1440
ggcggcggtg caaaaaacct tctgaaacg gcaacccgtg ctgaatggca gggaaaaacg 1500
ctgggtgaa caggacaggg cgtgtgttat cagtgtgta gogatcttyc tccactgaat 1560
tcgggtgagg aagcgaatca gcaaaaaacc ctgtttggac tgtttgtgta cggcaatatg 1620
ccagtccgct ggttaggacc gaaagcaacg taccatggca atatcctata gcccgacgtc 1680
acctgtacgc caaatccgca acgtaatgac agtgtaccaa cctggcgcca gatgacggac 1740
aaagccattg aattgttgat taaaaatgag aaaggtttt tccctgaagt tgaaggtgag 1800
tcaatcgata aabagatca tcttgagaat ccttctgggc aaattggcga gaagtctgat 1860
ctcgatgaag ccgtacaaac ggcgttgaaa ttogctaaaa aggaggtata caggttggtc 1920
atactcaacg ctgataccgc ccacgcacgc cagattgttg cgcgggatac caaanctccg 1980
ggctcaccac aggcgtctaa taccaaaagt ggcgcagtga tgggtgatag ttaacggaac 2040
tcggaagagg attcacaaga acataccggc agtcagttgc gtattgggcg gtatggcccg 2100
catgcgctca atgttgttg actgacccgc cagaccgata tctttctaac catgaaagcc 2160
gtcttggggg atatgcaca ccatacccat caccattaa 2199

```

4210-91

4211-791

4212-PRT



<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 90

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly  
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly  
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu  
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr  
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp  
100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn  
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser  
130 135 140

Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp  
145 150 155 160

Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln  
165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly  
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys  
195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg  
210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro  
225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu  
245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala  
260 265 270

Ala Ala Ala Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala  
275 280 285

Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp  
290 295 300

Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn  
 305 310 315 320  
 Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala  
 325 330 335  
 Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp  
 340 345 350  
 Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys  
 355 360 365  
 Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala  
 370 375 380  
 Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile  
 385 390 395 400  
 His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly  
 405 410 415  
 Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro  
 420 425 430  
 Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser  
 435 440 445  
 Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys  
 450 455 460  
 Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu  
 465 470 475 480  
 Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp  
 485 490 495  
 Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu  
 500 505 510  
 Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln  
 515 520 525  
 Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp  
 530 535 540  
 Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val  
 545 550 555 560  
 Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala  
 565 570 575  
 Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly  
 580 585 590  
 Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala  
 595 600 605  
 Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala  
 610 615 620  
 Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val  
 625 630 635 640

Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp  
 645 650 655  
 Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala  
 660 665 670  
 Val Met Val Met Ser Tyr Gly Asn Ser Gln Glu Asp Ser Gln Glu His  
 675 680 685  
 Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn  
 690 695 700  
 Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala  
 705 710 715 720  
 Ala Leu Gly Asp Ile Ala His His His His His His  
 725 730

<210> 91  
 <211> 97+  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:scFv region

<400> 91  
 atgaaataacc tattgcctac ggcagccgct ggattgttat tactcgoggc ccagccggcc 60  
 atgggggagg tgaagctggt ggagctctgg ggagcttag tgaagctggt agggctccctg 120  
 caactctctt gtgcagcttc tggattcaact ttcagtagct ataccatgtc ttgggttcgc 180  
 cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggngg tagttccacc 240  
 tccctccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc 300  
 ctgtaccctg aatgagcag tctgaggtct gaggacacag ccattgtatta ctgtacaaga 360  
 agggggggtg gtttcaacct caactggtac ttgatgtct ggggcgcagg aacctcagtc 420  
 accgtctctt caggtggagg cggttcaggt gggcgcgctt ctggcggtgg cggatcggac 480  
 attgtgtga cacagtntcc agcttctttg gctgtgtctc tagggcagag ggccaccata 540  
 tcttcagag ccagtgaag tgttgatagt tatggctata attttatgca ctggtatcag 600  
 cagataccag gacagccacc caaactcttc atctatctgt catccaaact agagtctggg 660  
 atctctgcca gtttcagtg cagtgggtct aggcagact tcaacctcag cattaatctt 720  
 atgggggtg angatgttgc aacctattac tgcagcaaaa gtaatgagga tccgctcagc 780  
 ttcggtactg gacacagact gaaaataaaa cggcgggccg caccgaagcc ttccactccg 840  
 cccgggtctt cccgtatgaa acagctggaa gacaaagtag aggagctctt tagcaagaac 900  
 tccatctag aaaaagaggt agctcgtctg aaaaagctt ttggtgaacg tgggtggtac 960  
 catcacctc accattaa 978

<210> 92  
 <211> 325  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:scFv region

<400> 92  
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
 1 5 10 15  
 Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly  
 20 25 30  
 Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu  
 50 55 60  
 Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr  
 65 70 75 80  
 Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
 85 90 95  
 Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp  
 100 105 110  
 Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn  
 115 120 125  
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser  
 130 135 140  
 Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp  
 145 150 155 160  
 Ile Val Leu Thr Gln Xaa Pro Ala Ser Leu Ala Val Ser Leu Gly Gln  
 165 170 175  
 Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly  
 180 185 190  
 Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys  
 195 200 205  
 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg  
 210 215 220  
 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro  
 225 230 235 240  
 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu  
 245 250 255  
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala  
 260 265 270  
 Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln  
 275 280 285  
 Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu  
 290 295 300  
 Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His  
 305 310 315 320  
 His His His His His  
 325

&lt;210&gt; 93

&lt;211&gt; 2190

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of the artificial sequence:scFv region.

<400> 23

```

atganatacc tattgootac ggcagcgcgt ggcattgttat tactcgcggc ccagcccgcc 61
atgggcgcagg ttcagcttcca gcagtcttggg cctgcagctgg tgaagcccg ggccctcagtg 120
aagatttccot gcaaaagcttc tgggtacgca ttcagtagct cttggatgaa ctgggtggaag 180
caga ggcctg gacagggctct tgaatggatt ggcagcattt atcctggaaa tggagatact 240
aactacaatg ggaagtcca ggcgaaggcc acactgactg cagacaaatc ctccagcaca 300
gcctacatgc agctcagcag cctgacctct gtagactctg cgtctctatt ctgtgcagat 360
ggtaacctat attactatgc tatggactac tggggtcag gaaactcagt caccgtctcc 420
tcaggttgag ggggttcagg tgggcgcgc cctgggcgtg gcggatcgca aattgtcttc 480
accagctctc ctgcttccct agctgtatct ctggggcaga gggccacct ctcatgcagg 540
gcacacaaa gtgtcagtag atctggctat agttatatgc actggtacca acagaaacca 600
ggacagccac ccaaaactct catctatctt gcatccaaac tagaatctgg ggtccctgct 660
aggttcagtg gcagtgggtc tgggcacagac ttcacctcca acatccatcc tgtggaggag 720
gaggatgctg caacctatta ctgtcagcac agtagggagc ttcctcggac gttcgttggg 780
ggcaccacagg tggaaatcaa acgggcggcc gcagcccggg caccagaaat gcctgttctg 840
gaaaaaccgg ctgtctcagg cgtatattact gcacccggcg ggtctcgccg ttttaacgggt 900
gacacagctg cgtctctgct gattctctct agcgataaac ctgcaaaaaa tattattctt 960
ctgattggcg atgggtatgg ggcactggaa ataacctgcg caagttaata tgcggaaggt 1020
gggggcggct tttttaaagg tatagatgcc ttacgcctta cggggcaata caactcactat 1080
ggcctgaata aaaaaaccgg caaacccgac taactcaacg actcggcgc atcagcaaac 1140
gcctgttcaa cgggtgtcaa aactataaac gggcgctgg ggtcgatat tcaagaaaaa 1200
gacaccccaa gattcttggg aatggcaaaa gcgcaggtc tggcgacggg taactttct 1260
acgcagagct tgcaggatgc cagcccgctt ggcgtgggtg cacatgtgac ctgcgcgaaa 1320
tgttaaggct cgcgcgcgac cagtgaaaaa tgcgcgggta acgtcttggg aaaaaggcgg 1380
aaagatctga ttacgcaaca gctgttaaac gctcgtgcgc acgttactgt tggcgcgccc 1440
gcaaaaaact ttgtgaaa gcgaacgcct ggtgaatggc agggaaaaaa gctgtgtgaa 1500
caggaacagg cgggtgggta tcagttgggt agcgatgctg cctcactgaa ttgggtgag 1560
gaagcgaata agcaaaaaac cctgtctggc ctgtttgctg acggcaatat gcagtgccg 1620
tggctaggac cgaaggcaac gtacatggc aatatcgata agcccgagc cactctgacg 1680
ccaaatcgcg aactgaatga cagtgtacca acctgggcgc agatgacga caaagccatt 1740
gaattgttga gtaaaaaatg gaaaggcttc ttcctgcaag ttgaaygtgc gtcaatcgat 1800
aaacaggatc atgtgtcgaa tcttgggtgg caaatggcg agacggtoga tctcgatgaa 1860
gcgtaacaa gcggcgctgga attcgtctaa agggagggtg acacgctggt catagtcaac 1920
gttgatcaac cccacgcgag ccagattgtt ggcgcggata ccaagctcc gggcctcacc 1980
caggcgctaa atacaaaaga tgggcagtg atggtgatga gttacgggaa ctccgaagag 2040
gattacaaag aacataccgg cagtcagttg cgtattggcg cgtatggccc gcattgcgcc 2100
aatgttgtt gactgacgga ccagacgat ctctcttaca ccattgaaagc cgtctggtgg 2160
gatatcgac accatcacca tcaacattaa 2190

```

<211> 94

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 24

```

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
  1             5             10             15

Ala Gln Pro Ala Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
          20             25             30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
          35             40             45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
          50             55             60

```

Gln	Gly	Leu	Glu	Trp	Ile	Gly	Arg	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	
65					70					75						80
Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	
				85					90					95		
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Val	Asp	
			100					105					110			
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Asp	Gly	Asn	Val	Tyr	Tyr	Tyr	Ala	Met	
	115						120					125				
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	
130						135					140					
Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ile	Val	Leu	
145					150					155					160	
Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	
				165					170					175		
Ile	Ser	Cys	Arg	Ala	Ser	Lys	Ser	Val	Ser	Thr	Ser	Gly	Tyr	Ser	Tyr	
		180						185					190			
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	
	195						200					205				
Tyr	Leu	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	
210					215						220					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	
225					230					235					240	
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Ser	Arg	Glu	Leu	Pro	Arg	
				245					250					255		
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Ala	
		260						265					270			
Arg	Ala	Pro	Glu	Met	Pro	Val	Leu	Glu	Asn	Arg	Ala	Ala	Gln	Gly	Asp	
		275					280					285				
Ile	Thr	Ala	Pro	Gly	Gly	Ala	Arg	Arg	Leu	Thr	Gly	Asp	Gln	Thr	Ala	
	290					295					300					
Ala	Leu	Arg	Asp	Ser	Leu	Ser	Asp	Lys	Pro	Ala	Lys	Asn	Ile	Ile	Leu	
305					310					315					320	
Leu	Ile	Gly	Asp	Gly	Met	Gly	Asp	Ser	Glu	Ile	Thr	Ala	Ala	Arg	Asn	
			325					330						335		
Tyr	Ala	Glu	Gly	Ala	Gly	Gly	Phe	Phe	Lys	Gly	Ile	Asp	Ala	Leu	Pro	
		340						345					350			
Leu	Thr	Gly	Gln	Tyr	Thr	His	Tyr	Ala	Leu	Asn	Lys	Lys	Thr	Gly	Lys	
		355					360					365				
Pro	Asp	Tyr	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	Thr	Ala	Trp	Ser	Thr	
	370					375					380					
Gly	Val	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	Val	Asp	Ile	His	Glu	Lys	
385					390					395					400	

Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr  
 405 410 415  
 Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu  
 420 425 430  
 Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser  
 435 440 445  
 Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile  
 450 455 460  
 Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly  
 465 470 475 480  
 Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys  
 485 490 495  
 Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp  
 500 505 510  
 Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu  
 515 520 525  
 Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro  
 530 535 540  
 Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr  
 545 550 555 560  
 Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr  
 565 570 575  
 Asp Lys Ala Ile Gln Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu  
 580 585 590  
 Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro  
 595 600 605  
 Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg  
 610 615 620  
 Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr  
 625 630 635 640  
 Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala  
 645 650 655  
 Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val  
 660 665 670  
 Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Gln His Thr Gly Ser  
 675 680 685  
 Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly  
 690 695 700  
 Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly  
 705 710 715 720  
 Asp Ile Ala His His His His His His  
 725

<210> 95  
 <211> 969  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:scFv region

<400> 95  
 atgaataacc tattgcoctac ggcagccgct ggattgttat tactcgcggc ccagccgggc 60  
 atgg ggagg ttcagcttca gaagtctgga cctgagctgg tgaagccggg ggctcagtg 120  
 aaga'ttctc gaaaagcttc tggctacgca ttcagttagc ctgggatgaa ctgggtgaag 180  
 caga'gcoctg gacagggctc tgaagtggatt ggaaggattt atcttggaaa tggagatact 240  
 aact'caatg ggaagtcca gggbaaggcc acactgactg cagacaaatc ctccagcaca 300  
 gctc'catgc agctcagcag cctgacctct gtggactctg cggctctatt ctgtgcagat 360  
 ggta'cgtat attactatgc tatggaactac tggggccaag gaaactcagt cacgctctcc 420  
 tcaggtggag ggggttcagg tggcgcgcc cctggcggtg ggggacgca aattgttctc 480  
 accc'gtctc ctgcttctct agctgtatct ctggggcaga gggccacct ctcatgcagg 540  
 gccac'caaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaaaca 600  
 ggac'ggccac ccaaaactcct catctatctt gcatccaaac tagaatctgg ggtccctgcc 660  
 aggt'cagtg gaagtgggtc tgggacagac ttcacctca acatccatcc tgtggaggag 720  
 gagg'tgctg caacctatta ctgtcagcac agtagggagc ttcctcggac gttcggtgga 780  
 gypa'caagc tggaaatcaa acggggcgcc gcacccaagc ctccactcc gcccggtct 840  
 tccc'tatga aacagctgga agacaaagta gaggagctcc ttagcaagaa ctaccatcta 900  
 gaaa'cgagg tagctcgtct gaaaaagctt gttggtgaac gtggtggtea ccataccat 960  
 cacc'cttaa 969

<210> 96  
 <211> 322  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:scFv region

<400> 96  
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
 1 5 10 15  
 Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu  
 20 25 30  
 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly  
 35 40 45  
 Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly  
 50 55 60  
 Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr  
 65 70 75 80  
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys  
 85 90 95  
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp  
 100 105 110  
 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met  
 115 120 125  
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly



133	135	140
Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu		
145	150	155 160
Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr		
	165	170 175
Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr		
	180	185 190
Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile		
	195	200 205
Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly		
	210	215 220
Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu		
	225	230 235 240
Ile Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg		
	245	250 255
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro		
	260	265 270
Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp		
	275	280 285
Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val		
	290	295 300
Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His His		
	305	310 315 320
His His		

<110> 97  
 <111> 270  
 <112> DNA  
 <113> Artificial Sequence

<120>  
 <121> Description of the artificial sequence:scFv region

<110> 97  
 caggaaacag ctatgaccat gattacgcca agtttcacatg aaaatttat ttcaaggaga 60  
 cagtcataat gaaataccta ttgctaagg cagcgcctgg attgttatta ctgcggggcc 120  
 acccggccat ggcccaggtg cagctgcagg cgggcctgca ggtcgacctc gagatcaaac 180  
 jggggggccc agaacaaaaa ctcatctcag aagaggatct gaatggggcg gcacatcac 240  
 atcaccatca ctaataagaa ttcactggcc 270

<110> 98  
 <111> 61  
 <112> PRT  
 <113> Artificial Sequence

<120>  
 <121> Description of the artificial sequence:scFv region

<400> 96

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu Gln Val  
20 25 30

Asp Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu  
35 40 45

Ala Asp Leu Asn Gly Ala Ala His His His His His His  
50 55 60

<111> 99

<111> 888

<111> DNA

<111> Artificial Sequence

<120>

<120> Description of the artificial sequence:scFv region

<400> 99

atgaatatac tattgctac ggcagccgct ggattgttat tactcgcggc ccagccgggc 60  
atggccgagc tgaagctggt ggagtctggg ggaggcttag tgaagcctgg agggctccctg 120  
aaactctcct gtgcagccctc tggattcact ttcagtagct ataccatgtc ttgggttcgc 180  
cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggngg tagttccacc 240  
tactatccag acagtgtgaa gggccgatto accatctcca gagacaatgc caagaacacc 300  
ctgtccctgc aaatgagcag tctgaggtct gaggacacag ccattgtatta ctgtacaaga 360  
gaggggggtg gtttcacagt caactggtag ttgatgtct ggggggcagg aacctcagtc 420  
acagctctct caggtggagg cgggttcaggt gggggcgct ctgggggttg cggatcggac 480  
atttgcttga cacagtctcc agctctcttg gctgtctctc tagggagag ggcaccata 540  
tcttgcagag ccagtgaag tcttgatagt tatggctata attttatgca ctggtatcag 600  
cagatccag gacagccacc caaactcctc atctacgtg catccaacct agagtctggg 660  
atcctgcca ggttcagtg cagtgggtct aggcagact tcacctcac cattaatcct 720  
ctggaggctg atgatgttg aacctattac tctcagcaaa gtaatgagga tccgtcacg 780  
ttcggctcag ggaacagact ggaataaaa cgggcggcgg cagaacaaaa actcatctca 840  
gaagaggctc tgaatggggc ggcacatcac catcaccata actaataa 888

<110> 100

<111> 204

<111> PRT

<111> Artificial Sequence

<120>

<120> Description of the artificial sequence:scFv region

<400> 100

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly  
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly  
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu  
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr  
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
 85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp  
 100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn  
 115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser  
 130 135 140

Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp  
 145 150 155 160

Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln  
 165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly  
 180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys  
 195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg  
 210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro  
 230 235 240

Val Gln Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu  
 245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala  
 260 265 270

Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 275 280 285

His His His His His His  
 290

0110: 101

0111: 876

0112: DNA

0113: Artificial Sequence

0120:

0123: Description of the artificial sequence: scFv region

0400: 101

atgaaataac tattgctac ggcagcgcgt ggattgttat tactggggg ccagccggcc 60  
 atggccggagg ttcagcttca gcagctctga cctgagctgg tgaagcccg ggccctcagtg 120  
 agtatttctt gcaaaagcttc tggctacgca ttcagtagct cttggatgaa ctgggtgaag 180  
 ccagaggcctg gacagggtct tgaatggatt ggaaggattt atcctggaaa tggagatact 240  
 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 300  
 gctacatgca agctcagcag cctgacctct gtggactctg cggctctatt ctgtgcagat 360  
 ggtaacgtat attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 420  
 tcaggtggag ggggttcagg tggggcgccc tctggcggtg ggggatcgca aattgttctc 480  
 acccagttct ctgcttctct agctgtatct ctgggcgaga gggcaccat ctcatgcagg 540  
 gccagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaaacca 600

ggacagccac ccaaaactcct catctatctt gcacccaacc tagaatctgg ggtccctgca 660  
 aggttcagtg gcagtggggc tgggacagac ttcaccccca acatccatcc tggggaggag 720  
 gaggatgctg caacctatta ctgtcagcac agtagggagc ttccctggac gttcgggtga 780  
 ggcaccaagc tggaaatcaa acgggggggc gcagaacaaa aactcatctc agaagaggat 840  
 ctgaatgggg cggcacatca ccacaccat tactaa 876

<210> 102

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 102

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
 1 5 10 15  
 Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu  
 20 25 30  
 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly  
 35 40 45  
 Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly  
 50 55 60  
 Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr  
 65 70 75 80  
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys  
 85 90 95  
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp  
 100 105 110  
 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met  
 115 120 125  
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly  
 130 135 140  
 Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu  
 145 150 155 160  
 Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr  
 165 170 175  
 Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr  
 180 185 190  
 Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile  
 195 200 205  
 Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly  
 210 215 220  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu  
 225 230 235 240  
 Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg  
 245 250 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu  
 260 265 270

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His  
 275 280 285

His His His  
 290

<210> 103  
 <211> 74  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:primer

<400> 103  
 ggcccgagaa caaaaactca tctcagaaga ggatctgaat gggcgggcac atcaccatca 60  
 cactactaa taag 74

<210> 104  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:primer

<400> 104  
 ttattagtga tggatgatgg gatgtgccgc cccattcaga tctcttcttg agatgagttt 60  
 ttgttctgc 69

<210> 105  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:CDR3 region

<400> 105  
 Cys Xaa Xaa Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Xaa Xaa Cys  
 1 5 10 15

<210> 106  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of the artificial sequence:CDR3 region

<400> 106  
 Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp  
 1 5 10 15